

## SEQUENCE LISTING

<110> Genox Research, Inc.

National Center for Child Health and Development

<120> Methods for examination for allergic diseases, and drugs for  
treating allergic diseases

<130> G1-A0212-US

<140>

<141>

<150> JP 2002-188490

<151> 2002-06-27

<160> 18

<170> PatentIn Ver. 2.0

<210> 1

<211> 3794

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (730)..(2607)

<400> 1

ataaatgacg tgccgagaga gcgagcgaac ggcgcggccgg gagagcggag ttcctgcct 60

cccgcccccc acccctccag ctcctgtcc tcctccgctc cccatacaca gacgcgccta 120

cacccgctcc ctcactcgca cacacagaca caagcgcgca cacaggctcc gcacacacac 180

ttgcgtctcc cgcgctca caccctctt gccctgagcc cttgccggtg cagcgccg 240  
 ccgcagctgg acgccccctcc cgggctcaact ttgcaacgct gacggtgccg gcagtgccg 300  
 tggaggtggg aacagcggcg gcatcctccc ccctggtcac agcccaagcc aggacgccc 360  
 cggAACCTCT cggctgtgct ctcccattgag tcgggatcgc agcatcccc accagccct 420  
 caccgcctcc gggagccgct gggcttgc accgcagccc ttccgggaca gcagctgtga 480  
 ctccccccca gtgcagattt cggacagact ctctagaaac tcgctctaaa gacggaaccg 540  
 ccacagcact caaagcccac tgcgaaagag ggcagccggg caagccggg ccctgaggct 600  
 ggacccttag cggtgccggg cagcactgcc ggcgcttcgc ctgcggac gtccgctct 660  
 cctacactct cagcctccgc tggagagacc cccagcccca ccattcagcg cgcaagatac 720  
 cctccagat atg ccc tgc gtc caa gcc caa tat agc cct tcc cct cca ggt 771  
 Met Pro Cys Val Gln Ala Gln Tyr Ser Pro Ser Pro Pro Gly  
 1 5 10  
 tcc agt tat gcg gcg cag aca tac agc tcg gaa tac acc acg gag atc 819  
 Ser Ser Tyr Ala Ala Gln Thr Tyr Ser Ser Glu Tyr Thr Thr Glu Ile  
 15 20 25 30  
 atg aac ccc gac tac acc aag ctg acc atg gac ctt ggc agc act gag 867  
 Met Asn Pro Asp Tyr Thr Lys Leu Thr Met Asp Leu Gly Ser Thr Glu  
 35 40 45  
 atc acg gct aca gcc acc acg tcc ctg ccc agc atc agt acc ttc gtg 915  
 Ile Thr Ala Thr Ala Thr Ser Leu Pro Ser Ile Ser Thr Phe Val  
 50 55 60  
 gag ggc tac tcg agc aac tac gaa ctc aag cct tcc tgc gtg tac caa 963  
 Glu Gly Tyr Ser Ser Asn Tyr Glu Leu Lys Pro Ser Cys Val Tyr Gln

65	70	75	
atg cag cgg ccc ttg atc aaa gtg gag gag ggg cgg gcg ccc agc tac			1011
Met Gln Arg Pro Leu Ile Lys Val Glu Glu Gly Arg Ala Pro Ser Tyr			
80	85	90	
cat cac cat cac cac cac cac cac cac cat cac cag cag			1059
His Gln Gln			
95	100	105	110
cag cat cag cag cca tcc att cct cca gcc tcc agc ccg gag gac gag			1107
Gln His Gln Gln Pro Ser Ile Pro Pro Ala Ser Ser Pro Glu Asp Glu			
115	120	125	
gtg ctg ccc agc acc tcc atg tac ttc aag cag tcc cca ccg tcc acc			1155
Val Leu Pro Ser Thr Ser Met Tyr Phe Lys Gln Ser Pro Pro Ser Thr			
130	135	140	
ccc acc acg ccg gcc ttc ccc ccg cag gcg ggg gcg tta tgg gac gag			1203
Pro Thr Thr Pro Ala Phe Pro Pro Gln Ala Gly Ala Leu Trp Asp Glu			
145	150	155	
gca ctg ccc tcg gcg ccc ggc tgc atc gca ccc ggc ccg ctg ctg gac			1251
Ala Leu Pro Ser Ala Pro Gly Cys Ile Ala Pro Gly Pro Leu Leu Asp			
160	165	170	
ccg ccg atg aag gcg gtc ccc acg gtg gcc ggc gcg cgc ttc ccg ctc			1299
Pro Pro Met Lys Ala Val Pro Thr Val Ala Gly Ala Arg Phe Pro Leu			
175	180	185	190
ttc cac ttc aag ccc tcg ccg cat ccc ccc gcg ccc agc ccg gcc			1347
Phe His Phe Lys Pro Ser Pro Pro His Pro Pro Ala Pro Ser Pro Ala			
195	200	205	
ggc ggc cac cac ctc ggc tac gac ccg acg gcc gct gcc gcg ctc agc			1395
Gly Gly His His Leu Gly Tyr Asp Pro Thr Ala Ala Ala Leu Ser			

210	215	220	
ctg ccg ctg gga gcc gca gcc gcc ggc agc cag cgc gcc gcc ctt 1443			
Leu Pro Leu Gly Ala Ala Ala Ala Gly Ser Gln Ala Ala Ala Leu			
225	230	235	
gag agc cac ccg tac ggg ctg ccg ctg gcc aag agg ggc gcc ccg ctg 1491			
Glu Ser His Pro Tyr Gly Leu Pro Leu Ala Lys Arg Ala Ala Pro Leu			
240	245	250	
gcc ttc ccg cct ctc ggc ctc acg ccc tcc cct acc ggc tcc agc ctg 1539			
Ala Phe Pro Pro Leu Gly Leu Thr Pro Ser Pro Thr Ala Ser Ser Leu			
255	260	265	270
ctg ggc gag agt ccc agc ctg ccg tcg ccc agc agg agc tcg tcg 1587			
Leu Gly Glu Ser Pro Ser Leu Pro Ser Pro Pro Ser Arg Ser Ser			
275	280	285	
tct ggc gag ggc acg tgt gcc gtg tgc ggg gac aac gcc gcc tgc cag 1635			
Ser Gly Glu Gly Thr Cys Ala Val Cys Gly Asp Asn Ala Ala Cys Gln			
290	295	300	
cac tac ggc gtg cga acc tgc gag ggc tgc aag ggc ttt ttc aag aga 1683			
His Tyr Gly Val Arg Thr Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg			
305	310	315	
aca gtg cag aaa aat gca aaa tat gtt tgc ctg gca aat aaa aac tgc 1731			
Thr Val Gln Lys Asn Ala Lys Tyr Val Cys Leu Ala Asn Lys Asn Cys			
320	325	330	
cca gta gac aag aga cgt cga aac cga tgt cag tac tgt cga ttt cag 1779			
Pro Val Asp Lys Arg Arg Asn Arg Cys Gln Tyr Cys Arg Phe Gln			
335	340	345	350
aag tgt ctc agt gtt gga atg gta aaa gaa gtt gtc cgt aca gat agt 1827			
Lys Cys Leu Ser Val Gly Met Val Lys Glu Val Val Arg Thr Asp Ser			

355	360	365	
ctg aaa ggg agg aga ggt cgt ctg cct tcc aaa cca aag agc cca tta Leu Lys Gly Arg Arg Gly Arg Leu Pro Ser Lys Pro Lys Ser Pro Leu			1875
370	375	380	
caa cag gaa cct tct cag ccc tct cca cct tct cct cca atc tgc atg Gln Gln Glu Pro Ser Gln Pro Ser Pro Pro Ser Pro Pro Ile Cys Met			1923
385	390	395	
atg aat gcc ctt gtc cga gct tta aca gac tca aca ccc aga gat ctt Met Asn Ala Leu Val Arg Ala Leu Thr Asp Ser Thr Pro Arg Asp Leu			1971
400	405	410	
gat tat tcc aga tac tgt ccc act gac cag gct gct gca ggc aca gat Asp Tyr Ser Arg Tyr Cys Pro Thr Asp Gln Ala Ala Ala Gly Thr Asp			2019
415	420	425	430
gct gag cat gtgcaa caatttc tac aac ctc ctg aca gcc tcc att gat Ala Glu His Val Gln Gln Phe Tyr Asn Leu Leu Thr Ala Ser Ile Asp			2067
435	440	445	
gta tcc aga agc tgg gca gaa aag att ccg gga ttt act gat ctc ccc Val Ser Arg Ser Trp Ala Glu Lys Ile Pro Gly Phe Thr Asp Leu Pro			2115
450	455	460	
aaa gaa gat cag aca ttattt gaa tca gcc ttt ttg gag ctg ttt Lys Glu Asp Gln Thr Leu Leu Ile Glu Ser Ala Phe Leu Glu Leu Phe			2163
465	470	475	
gtc ctc aga ctt tcc atc agg tca aac act gct gaa gat aag ttt gtg Val Leu Arg Leu Ser Ile Arg Ser Asn Thr Ala Glu Asp Lys Phe Val			2211
480	485	490	
ttc tgc aat gga ctt gtc ctg cat cga ctt cag tgc ctt cgt gga ttt Phe Cys Asn Gly Leu Val Leu His Arg Leu Gln Cys Leu Arg Gly Phe			2259

495	500	505	510	
ggg gag tgg ctc gac tct att aaa gac ttt tcc tta aat ttg cag agc				2307
Gly Glu Trp Leu Asp Ser Ile Lys Asp Phe Ser Leu Asn Leu Gln Ser				
515	520	525		
ctg aac ctt gat atc caa gcc tta gcc tgc ctg tca gca ctg agc atg				2355
Leu Asn Leu Asp Ile Gln Ala Leu Ala Cys Leu Ser Ala Leu Ser Met				
530	535	540		
atc aca gaa aga cat ggg tta aaa gaa cca aag aga gtc gaa gag cta				2403
Ile Thr Glu Arg His Gly Leu Lys Glu Pro Lys Arg Val Glu Glu Leu				
545	550	555		
tgc aac aag atc aca agc agt tta aaa gac cac cag agt aag gga cag				2451
Cys Asn Lys Ile Thr Ser Ser Leu Lys Asp His Gln Ser Lys Gly Gln				
560	565	570		
gct ctg gag ccc acc gag tcc aag gtc ctg ggt gcc ctg gta gaa ctg				2499
Ala Leu Glu Pro Thr Glu Ser Lys Val Leu Gly Ala Leu Val Glu Leu				
575	580	585	590	
agg aag atc tgc acc ctc ggc ctc cag cgc atc ttc tac ctg aag ctg				2547
Arg Lys Ile Cys Thr Leu Gly Leu Gln Arg Ile Phe Tyr Leu Lys Leu				
595	600	605		
gaa gac ttg gtg tct cca cct tcc atc att gac aag ctc ttc ctg gac				2595
Glu Asp Leu Val Ser Pro Pro Ser Ile Ile Asp Lys Leu Phe Leu Asp				
610	615	620		
acc cta cct ttc taatcaggag cagtggagca gtgagctgcc tcctctccta				2647
Thr Leu Pro Phe				
625				
gcacctgctt gctacgcagc aaagggatag gttggaaac ctatcatttc ctgtccttcc				2707

ttaagaggaa aagcagctcc tgtagaaagc aaagacttc tttttttct ggctcttcc 2767  
cttacaacct aaagccagaa aacttgcaga gtattgtgtt ggggttgtt tttatattt 2827  
ggcattgggg gatgggggtgg gaggggggtta tagttcatga gggtttcta agaaattgct 2887  
aacaaagcac ttttggacaa tgctatccca gcaggaaaaaa aaaggataat ataactgtt 2947  
taaaaactctt tctgggaat ccaattatacg ttgcttgc tttaaaaaca agaacagcca 3007  
agggttgttc gccagggtag gatgtgtctt aaagattggt ccctgaaaa tatgcttcct 3067  
gtatcaaagg tacgtatgtg gtgcaaacaa ggcagaaact tcctttaat ttccttcctc 3127  
ctttatTTta acaaatggtg aaagatggag gattacctac aaatcagaca tggcaaaaca 3187  
ataatggctg tttgcttcca taaacaagtg caatTTTTta aagtgtgtc ttactaagtc 3247  
ttgtttatTA actctcctt attctatcg gaaataaaaaa ggaggcagtc atgttagcaa 3307  
atgacacgtt aatacccta gcagaggctg tggcacctt ccctgtcgat ccctctgag 3367  
gtatggccca tccaagactt ttaggccatt ctgtatggaa ccagatccct gccctgactg 3427  
tccagctatc ctgaaagtgg atcagattat aaactggatt acatgtact gttttgggg 3487  
tgttctatca accccaccag agttccctaa acttgcttca gttatagtaa ctgactggta 3547  
tattcattca gaagcgccat aagtcagttg agtatttgat ccctagataa gaacatgcaa 3607  
atcagcagga actggcata caggtaagc accagggaca ataaggattt ttatagatat 3667  
aatttaattt ttgttattgg ttaaggagac aattttggag agcaagcaa tcttttaaa 3727  
aaatagtatg aatgtgaata ctagaaaaga tttaaaaaat agtatgagtg tgagtactag 3787

gaaggat

3794

&lt;210&gt; 2

&lt;211&gt; 626

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

Met	Pro	Cys	Val	Gln	Ala	Gln	Tyr	Ser	Pro	Ser	Pro	Pro	Gly	Ser	Ser
1															
			5					10						15	

Tyr	Ala	Ala	Gln	Thr	Tyr	Ser	Ser	Glu	Tyr	Thr	Glu	Ile	Met	Asn
		20				25					30			

Pro	Asp	Tyr	Thr	Lys	Leu	Thr	Met	Asp	Leu	Gly	Ser	Thr	Glu	Ile	Thr
	35				40						45				

Ala	Thr	Ala	Thr	Thr	Ser	Leu	Pro	Ser	Ile	Ser	Thr	Phe	Val	Glu	Gly
	50				55				60						

Tyr	Ser	Ser	Asn	Tyr	Glu	Leu	Lys	Pro	Ser	Cys	Val	Tyr	Gln	Met	Gln
	65			70				75				80			

Arg	Pro	Leu	Ile	Lys	Val	Glu	Glu	Gly	Arg	Ala	Pro	Ser	Tyr	His	His
	85					90						95			

His	Gln	Gln	Gln	His											
	100				105				110						

Gln	Gln	Pro	Ser	Ile	Pro	Pro	Ala	Ser	Ser	Pro	Glu	Asp	Glu	Val	Leu
	115				120					125					

Pro	Ser	Thr	Ser	Met	Tyr	Phe	Lys	Gln	Ser	Pro	Pro	Ser	Thr	Pro	Thr
	130			135						140					

Thr Pro Ala Phe Pro Pro Gln Ala Gly Ala Leu Trp Asp Glu Ala Leu  
 145 150 155 160

Pro Ser Ala Pro Gly Cys Ile Ala Pro Gly Pro Leu Leu Asp Pro Pro  
 165 170 175

Met Lys Ala Val Pro Thr Val Ala Gly Ala Arg Phe Pro Leu Phe His  
 180 185 190

Phe Lys Pro Ser Pro Pro His Pro Pro Ala Pro Ser Pro Ala Gly Gly  
 195 200 205

His His Leu Gly Tyr Asp Pro Thr Ala Ala Ala Ala Leu Ser Leu Pro  
 210 215 220

Leu Gly Ala Ala Ala Ala Ala Gly Ser Gln Ala Ala Ala Leu Glu Ser  
 225 230 235 240

His Pro Tyr Gly Leu Pro Leu Ala Lys Arg Ala Ala Pro Leu Ala Phe  
 245 250 255

Pro Pro Leu Gly Leu Thr Pro Ser Pro Thr Ala Ser Ser Leu Leu Gly  
 260 265 270

Glu Ser Pro Ser Leu Pro Ser Pro Pro Ser Arg Ser Ser Ser Ser Gly  
 275 280 285

Glu Gly Thr Cys Ala Val Cys Gly Asp Asn Ala Ala Cys Gln His Tyr  
 290 295 300

Gly Val Arg Thr Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val  
 305 310 315 320

Gln Lys Asn Ala Lys Tyr Val Cys Leu Ala Asn Lys Asn Cys Pro Val  
 325 330 335

Asp Lys Arg Arg Arg Asn Arg Cys Gln Tyr Cys Arg Phe Gln Lys Cys  
340 345 350

Leu Ser Val Gly Met Val Lys Glu Val Val Arg Thr Asp Ser Leu Lys  
355 360 365

Gly Arg Arg Gly Arg Leu Pro Ser Lys Pro Lys Ser Pro Leu Gln Gln  
370 375 380

Glü Pro Ser Gln Pro Ser Pro Pro Ser Pro Pro Ile Cys Met Met Asn  
385 390 395 400

Ala Leu Val Arg Ala Leu Thr Asp Ser Thr Pro Arg Asp Leu Asp Tyr  
405 410 415

Ser Arg Tyr Cys Pro Thr Asp Gln Ala Ala Ala Gly Thr Asp Ala Glu  
420 425 430

His Val Gln Gln Phe Tyr Asn Leu Leu Thr Ala Ser Ile Asp Val Ser  
435 440 445

Arg Ser Trp Ala Glu Lys Ile Pro Gly Phe Thr Asp Leu Pro Lys Glu  
450 455 460

Asp Gln Thr Leu Leu Ile Glu Ser Ala Phe Leu Glu Leu Phe Val Leu  
465 470 475 480

Arg Leu Ser Ile Arg Ser Asn Thr Ala Glu Asp Lys Phe Val Phe Cys  
485 490 495

Asn Gly Leu Val Leu His Arg Leu Gln Cys Leu Arg Gly Phe Gly Glu  
500 505 510

Trp Leu Asp Ser Ile Lys Asp Phe Ser Leu Asn Leu Gln Ser Leu Asn  
515 520 525

Leu Asp Ile Gln Ala Leu Ala Cys Leu Ser Ala Leu Ser Met Ile Thr  
 530 535 540

Glu Arg His Gly Leu Lys Glu Pro Lys Arg Val Glu Glu Leu Cys Asn  
 545 550 555 560

Lys Ile Thr Ser Ser Leu Lys Asp His Gln Ser Lys Gly Gln Ala Leu  
 565 570 575

Glu Pro Thr Glu Ser Lys Val Leu Gly Ala Leu Val Glu Leu Arg Lys  
 580 585 590

Ile Cys Thr Leu Gly Leu Gln Arg Ile Phe Tyr Leu Lys Leu Glu Asp  
 595 600 605

Leu Val Ser Pro Pro Ser Ile Ile Asp Lys Leu Phe Leu Asp Thr Leu  
 610 615 620

Pro Phe  
 625

<210> 3  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Artificially  
 Synthesized Primer Sequence

<400> 3  
 gttttttttt tttttta

<210> 4

<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Artificially  
Synthesized Primer Sequence

<400> 4  
gtttttttt ttttttc

17

<210> 5  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Artificially  
Synthesized Primer Sequence

<400> 5  
gtttttttt ttttttg

17

<210> 6  
<211> 10  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Artificially  
Synthesized Primer Sequence

<400> 6  
cattctcagg

10

<210> 7  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Artificially  
Synthesized Primer Sequence

<400> 7  
tgcccttgtct agaactgcac ag 22

<210> 8  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Artificially  
Synthesized Primer Sequence

<400> 8  
aagtgtgttg gaccaaggcag c 21

<210> 9  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Artificially  
Synthesized Probe Sequence

<400> 9

aagtcagtgc agagcctgga tgagga

26

<210> 10

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially —  
Synthesized Primer Sequence

<400> 10

tcacccacac tgtgcccatc tacga

25

<210> 11

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
Synthesized Primer Sequence

<400> 11

cagcggAACc gctcattGCC aatgg

25

<210> 12

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
Synthesized Probe Sequence

<220>

<221> misc\_binding

<222> (1)

<223> Label FAM

<220>

<221> misc\_binding

<222> (7) —

<223> Label TAMRA

<400> 12

atgcctcccc ccatgccatc ctgcgt

26

<210> 13

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
Synthesized Primer Sequence

<400> 13

gttccaggca ataacatcat acc

23

<210> 14

<211> 23

<212> DNA

<213> Artificial Sequence

220

<223> Description of Artificial Sequence:Artificially  
Synthesized Primer Sequence

<400> 14

gctacttgtg aaactcccaa atg

23

<210> 15

2087

<212> DNA

<213> Homo sapiens

<400> 15

ggcaaaaatc tgtactttaa aaagtgcattt tggatgattc tttggcacac taaggtttga 60

gaaccatcga tatagtttat aataacaact caattttacc ttgaattttc cagttttcc 120

tggggttgag aagggtatgag caatagagat ataaatttc ctgaaagcaa tcaattcatt 180

taacaatatac ttactgaatg gctgcttaggt agtagggact gttccaggggc aatggacacg 240

ttgctgaaca agacaaaagcc ctatccaca tgaacctac atacctgtaa aggagaaaaa 300

gagtaaacaatatacaatt gcagtgtatgt cattgggtggg aggagaggaa ttttttgctt 360

tttgctttt ggagtgaaaaa catacgatgggggg gatcagaaaaaa gaaaaaaatttggggggggggaaat 420

atattcattg ccaatttta aaatgtcact ttttaaagtg taagaaccta agaatatgt 480

tacatagttt gacttataca atgatcacat ctaaaaatttt tagagctata gttgagaaaa 540

gtaacatttt aaggggagaa aaacgtgtcc ttagcgtagt ctacatattt agccagggct 600

gaaagtgaga tagagtaaat attagattcc actctgctat taaaggctca catcaactat 660

ttttgagggg tggtgtttc catgggtctc acttaatttc cacacaaata tctcatttg 720  
ggcctggcct attgctgaag tctgacttgt atagctgcgt tactgccata taaaacacac 780  
agacccattt tagtttacat aatatccatt gctgttgtt gcagctctag attcccatc 840  
taggtgctt agagaaacct tccttaggca ttggctgtca gtaaatgtaa tactgtgtct 900  
ttgacttagtg agaaaagccag agttctgaca gatcaataac ccctataggg tggaaaaaaa 960  
ttagtataaa cagaaaaaaa gttcacttaa aaaaatcttt ttgcatttga cctatgttcg 1020  
attggcatga tcagtaagca aatatttcta gattttctt gtcaaaccac aaacctactt 1080  
agcccagaga cagagcaatc aatgttagggc agcagagaca cagagctggg agtccagtc 1140  
ttccaactct aggaccagta ttcatgggt gaggtttcc taaactggta ggccaggcag 1200  
agaaaaaaatc taaaacgttt tggccgttc ctttacatct tatgtccaat agaggagatt 1260  
tttctttcc tccagcattt gatgctgacc ctccagtcac ccccaagttt ctggggcgtc 1320  
agactgaatt cactttggct cccaaattct gagacttgga cccaaaccac tgcaggtgaa 1380  
gcccagagga tctggctgga gcctggcagg ctggccggc tggcttcct tcttgctggg 1440  
ctccatcaga gaaaagtaca cacacagggc gggcagggc ttcacttccc tgtgtgcaga 1500  
aggcatgaaa tgtgagccca gcaggggcag aagcctgcag aggaccctgg gtgaaagcta 1560  
cacactttga tggattctga acaaataatttga gaagcagaga gattgtttag ttgtgagcca 1620  
tggattcagg ggagtcaatc caggaggtag ctgtcagatc catttcagg ggaaactattt 1680  
cattcttag tcttttctc tctccacta tttaaaaca aaataatgct gaatcagtgt 1740

caagttccag gcaataacat catacctggc gtgatTTAGC aatatttaga atcatttaat 1800  
gcaagagcca gaagtaatct tagggatcag gtagtccact ttattcctgt tccagagact 1860  
gaaactgact cagagaggTTT aaatgccttg tctagaactg cacagcaagt cagtgcagag 1920  
cctggatgag gaccccatga cctgctgctt ggtccaaacac actttcctt actcccactc 1980  
atTTgggagt ttcacaagta gctccctcag ctTTTgaaag ggaggatctg ccctgaattt 2040  
cattctgctc ttggagagcc tgtggaatta ttaaataaaat tcataaa 2087

<210> 16

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
Synthesized Primer Sequence

<400> 16

tgggtgcctt ggtagaact

19

<210> 17

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
Synthesized Primer Sequence

<400> 17

gcttcaggta gaagatgcgc t

21

&lt;210&gt; 18

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:Artificially  
Synthesized Probe Sequence

&lt;400&gt; 18

aggaagatct gcaccctggg cctc

24